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0129

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/022,025A

DATE: 01/22/2003

TIME: 13:51:43

Input Set : A:\Revised Sequence Listing.txt

Output Set: N:\CRF4\01222003\J022025A.raw

5 &lt;110&gt; APPLICANT: Coleman, John R.

9 &lt;120&gt; TITLE OF INVENTION: Nucleic Acid Molecules and Polypeptides for Catabolism of

Abcscisic

10 Acid

14 &lt;130&gt; FILE REFERENCE: 3310 0003

18 &lt;140&gt; CURRENT APPLICATION NUMBER: US 10/022,025A

C--&gt; 20 &lt;141&gt; CURRENT FILING DATE: 2003-01-09

24 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/254,819

26 &lt;151&gt; PRIOR FILING DATE: 2000-12-13

30 &lt;160&gt; NUMBER OF SEQ ID NOS: 8

34 &lt;170&gt; SOFTWARE: PatentIn version 3.0

38 &lt;210&gt; SEQ ID NO: 1

40 &lt;211&gt; LENGTH: 2009

42 &lt;212&gt; TYPE: DNA

44 &lt;213&gt; ORGANISM: Arabidopsis thaliana

48 &lt;220&gt; FEATURE:

50 &lt;221&gt; NAME/KEY: gene

52 &lt;222&gt; LOCATION: (1)..(2009)

56 &lt;400&gt; SEQUENCE: 1

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61 tatctctctc ttctcttcac ttactTTgct ttgatccgcc atggctacga aactcgaaag 180  
63 ctcccttaatc tttgcccttt tgtccaaatg cagcgTTcta agccaaacca acctgcctt 240  
65 ctccctcctc gccgtcacaa tcatctggct cgccatatct ctcttcttat ggacctatcc 300  
67 cggTggacct gctTgggga aatacctctt cggccggTTa atatccggtt catacaaac 360  
69 cggaaacggt attcccggTc caaaaggctt ccctTTggtt ggaagcatgt cactcatgtc 420  
71 aagcactcta gctcacgcac gaatcgctga tgcagctgag aaattcggag ccaagaggct 480  
73 catggctttc agcttaggag agactcgctg gatcgTcacg tgcaatcccg acgtagcgaa 540  
75 agagattctg aatagcccgg tttttgctga tgcaccggtt aaagaatcgg ctactcact 600  
77 gatgtttaac agagcaattg gttttgcacc acacggTgTT tactggcgaa cgcttcgccg 660  
79 tatcgcttcg aacctctctt ttagtataaa acaaTcaga agagccgaga cgcaacgcag 720  
81 agtgatctca agccagatgg ttgagtttct tgaaaaacag agtagtaacg aacctgTTT 780  
83 tgttcgtgag ttgcttaaaa cggcgTcgct taacaacatg atgtgctctg tattcgga 840  
85 agagtatgag cttgaaaaaa accatgttga gttacgtgaa atggtcgaag aaggTTatga 900  
87 tttgctcgga acgttgaaTT ggactgatca cttccttgg ctatcgaggt ttgatcctca 960  
89 aagactccgg tctagatgTT ccacactcgt accaaaggta aaccggTTTg tatcccggt 1020  
91 tatatccgaa caccgtaatc aaaccggTga tttgcctcgt gatttcgTcg acgttttTgct 1080  
93 ctccctccat ggTtcagata aattatccga ccggacata atcgccgTtc tttgggtatg 1140  
95 cacaccattt atttgattaa ttattcttaa ttatattTgt tgaaaattgc ttaggattat 1200  
97 ttagattaaa acatgaaatt tgagactcaa tgtgacgtgt tgtggaataa ttaaagcatt 1260  
99 agaagttttt tgtttgacat caaattagta aattttagat ttataacag tttctataaa 1320  
101 aagtaaaaag tactaaaatt tttgagttat tattacagga gatgatattc agaggaacag 1380  
103 acacagttgc ggtcttaatc gagtggatcc tcgctaggat ggtccttcac ccagatatgc 1440  
105 aatcaacggt acaaacgcag ctggatcaag tagtcgggaa atcaagagcc ctagatgaat 1500

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109 ctccaggccc acttctatca tgggccggt tggccataac agacacgatc gttgatggtc 1620
111 gtcttggtcc ggcaggacc acagcaatgg tgaacatgtg ggccgtatcg catgatccac 1680
113 acgtgtgggt tgatcctttg gagtttaaac ctgagagggt cgtggcaaaa gaaggtagg 1740
115 tggagttttc ggttcttggg tcgatttga gacttgcacc tttcgggtcg ggtcgtcgga 1800
117 tttgcccggg gaagaatctt ggttttacta ccggtatggt ttggacggcg atgatgttac 1860
119 atgagtttga atggggaccg tccgatggta acggcggttga cttatctgag aaactgaggc 1920
121 tttcttgcca gatggcta cctcttctg ctaaattgcg ccgtaggcgc agttaaaaaa 1980
123 aagaagctca tatgagaatt agagatttt 2009
126 <210> SEQ ID NO: 2
128 <211> LENGTH: 1593
130 <212> TYPE: DNA
132 <213> ORGANISM: Arabidopsis thaliana
136 <220> FEATURE:
138 <221> NAME/KEY: CDS
140 <222> LOCATION: (1)..(1593)
144 <400> SEQUENCE: 2
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146 Met Ala Thr Lys Leu Glu Ser Ser Leu Ile Phe Ala Leu Leu Ser Lys
147 1 5 10 15
149 tgc agc gtt cta agc caa acc aac ctt gcc ttc tcc ctc ctc gcc gtc 96
150 Cys Ser Val Leu Ser Gln Thr Asn Leu Ala Phe Ser Leu Leu Ala Val
151 20 25 30
153 aca atc atc tgg ctc gcc ata tct ctc ttc tta tgg acc tat ccc ggt 144
154 Thr Ile Ile Trp Leu Ala Ile Ser Leu Phe Leu Trp Thr Tyr Pro Gly
155 35 40 45
157 gga cct gct tgg ggg aaa tac ctc ttc ggc cgg tta ata tcc ggt tca 192
158 Gly Pro Ala Trp Gly Lys Tyr Leu Phe Gly Arg Leu Ile Ser Gly Ser
159 50 55 60
161 tac aaa acc gga aac gtt att ccc ggt cca aaa ggc ttc cct ttg gtt 240
162 Tyr Lys Thr Gly Asn Val Ile Pro Gly Pro Lys Gly Phe Pro Leu Val
163 65 70 75 80
165 gga agc atg tca ctc atg tca agc act cta gct cac cga cga atc gct 288
166 Gly Ser Met Ser Leu Met Ser Ser Thr Leu Ala His Arg Arg Ile Ala
167 85 90 95
169 gat gca gct gag aaa ttc gga gcc aag agg ctc atg gct ttc agc tta 336
170 Asp Ala Ala Glu Lys Phe Gly Ala Lys Arg Leu Met Ala Phe Ser Leu
171 100 105 110
173 gga gag act cgc gtg atc gtc acg tgc aat ccc gac gta gcg aaa gag 384
174 Gly Glu Thr Arg Val Ile Val Thr Cys Asn Pro Asp Val Ala Lys Glu
175 115 120 125
177 att ctg aat agc ccg gtt ttt gct gat cga ccg gtt aaa gaa tcg gct 432
178 Ile Leu Asn Ser Pro Val Phe Ala Asp Arg Pro Val Lys Glu Ser Ala
179 130 135 140
181 tac tca ctg atg ttt aac aga gca att ggt ttt gca cca cac ggt gtt 480
182 Tyr Ser Leu Met Phe Asn Arg Ala Ile Gly Phe Ala Pro His Gly Val
183 145 150 155 160
185 tac tgg cga acg ctt cgc cgt atc gct tcg aac cat ctc ttt agt aca 528
186 Tyr Trp Arg Thr Leu Arg Arg Ile Ala Ser Asn His Leu Phe Ser Thr

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189	aaa	caa	atc	aga	aga	gcc	gag
190	Lys	Gln	Ile	Arg	Arg	Ala	Glu
191				180		185	
193	atg	gtt	gag	ttt	ctt	gaa	aaa
194	Met	Val	Glu	Phe	Leu	Glu	Lys
195				195		200	
197	cgt	gag	ttg	ctt	aaa	acg	gcg
198	Arg	Glu	Leu	Leu	Lys	Thr	Ala
199				210		215	
201	ttc	gga	caa	gag	tat	gag	ctt
202	Phe	Gly	Gln	Glu	Tyr	Glu	Leu
203	225					230	
205	atg	gtc	gaa	gaa	ggt	tat	gat
206	Met	Val	Glu	Glu	Gly	Tyr	Asp
207						245	
209	cac	ctt	cct	tgg	cta	tcg	gag
210	His	Leu	Pro	Trp	Leu	Ser	Glu
211						260	
213	tgt	tcc	aca	ctc	gta	cca	aag
214	Cys	Ser	Thr	Leu	Val	Pro	Lys
215						275	
217	tcc	gaa	cac	cgt	aat	caa	acc
218	Ser	Glu	His	Arg	Asn	Gln	Thr
219						290	
221	gtt	ttg	ctc	tcc	ctc	cat	ggt
222	Val	Leu	Leu	Ser	Leu	His	Gly
223	305					310	
225	atc	gcc	gtt	ctt	tgg	gag	atg
226	Ile	Ala	Val	Leu	Trp	Glu	Met
227						325	
229	gtc	tta	atc	gag	tgg	atc	ctc
230	Val	Leu	Ile	Glu	Trp	Ile	Leu
231						340	
233	caa	tca	acg	gta	caa	aac	gag
234	Gln	Ser	Thr	Val	Gln	Asn	Glu
235						355	
237	gcc	cta	gat	gaa	tct	gac	ttg
238	Ala	Leu	Asp	Glu	Ser	Asp	Leu
239						370	
241	gtg	aaa	gaa	gta	ttg	agg	ctt
242	Val	Lys	Glu	Val	Leu	Arg	Leu
243	385					390	
245	gcc	cgt	ttg	gcc	ata	aca	gac
246	Ala	Arg	Leu	Ala	Ile	Thr	Asp
247						405	
249	gca	ggg	acc	aca	gca	atg	gtg
250	Ala	Gly	Thr	Thr	Ala	Met	Val
251						420	

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253 cac gtg tgg gtt gat cct ttg gag ttt aaa cct gag agg ttc gtg gca      1344
254 His Val Trp Val Asp Pro Leu Glu Phe Lys Pro Glu Arg Phe Val Ala
255          435          440          445
257 aaa gaa ggt gag gtg gag ttt tcg gtt ctt ggg tcg gat ttg aga ctt      1392
258 Lys Glu Gly Glu Val Glu Phe Ser Val Leu Gly Ser Asp Leu Arg Leu
259          450          455          460
261 gca cct ttc ggg tcg ggt cgt cgg att tgc ccc ggg aag aat ctt ggt      1440
262 Ala Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Lys Asn Leu Gly
263 465          470          475          480
265 ttt act acc gtt atg ttt tgg acg gcg atg atg tta cat gag ttt gaa      1488
266 Phe Thr Thr Val Met Phe Trp Thr Ala Met Met Leu His Glu Phe Glu
267          485          490          495
269 tgg gga ccg tcc gat ggt aac ggc gtt gac tta tct gag aaa ctg agg      1536
270 Trp Gly Pro Ser Asp Gly Asn Gly Val Asp Leu Ser Glu Lys Leu Arg
271          500          505          510
273 ctt tct tgc gag atg gct aat cct ctt cct gct aaa ttg cgc cgt agg      1584
274 Leu Ser Cys Glu Met Ala Asn Pro Leu Pro Ala Lys Leu Arg Arg Arg
275          515          520          525
277 cgc agt taa
278 Arg Ser
279          530
282 <210> SEQ ID NO: 3
284 <211> LENGTH: 530
286 <212> TYPE: PRT
288 <213> ORGANISM: Arabidopsis thaliana
292 <400> SEQUENCE: 3
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298 Cys Ser Val Leu Ser Gln Thr Asn Leu Ala Phe Ser Leu Leu Ala Val
299          20          25          30
302 Thr Ile Ile Trp Leu Ala Ile Ser Leu Phe Leu Trp Thr Tyr Pro Gly
303          35          40          45
306 Gly Pro Ala Trp Gly Lys Tyr Leu Phe Gly Arg Leu Ile Ser Gly Ser
307          50          55          60
310 Tyr Lys Thr Gly Asn Val Ile Pro Gly Pro Lys Gly Phe Pro Leu Val
311 65          70          75          80
314 Gly Ser Met Ser Leu Met Ser Ser Thr Leu Ala His Arg Arg Ile Ala
315          85          90          95
318 Asp Ala Ala Glu Lys Phe Gly Ala Lys Arg Leu Met Ala Phe Ser Leu
319          100          105          110
322 Gly Glu Thr Arg Val Ile Val Thr Cys Asn Pro Asp Val Ala Lys Glu
323          115          120          125
326 Ile Leu Asn Ser Pro Val Phe Ala Asp Arg Pro Val Lys Glu Ser Ala
327          130          135          140
330 Tyr Ser Leu Met Phe Asn Arg Ala Ile Gly Phe Ala Pro His Gly Val
331 145          150          155          160
334 Tyr Trp Arg Thr Leu Arg Arg Ile Ala Ser Asn His Leu Phe Ser Thr
335          165          170          175
338 Lys Gln Ile Arg Arg Ala Glu Thr Gln Arg Arg Val Ile Ser Ser Gln

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339          180          185          190
342 Met Val Glu Phe Leu Glu Lys Gln Ser Ser Asn Glu Pro Cys Phe Val
343          195          200          205
346 Arg Glu Leu Leu Lys Thr Ala Ser Leu Asn Asn Met Met Cys Ser Val
347          210          215          220
350 Phe Gly Gln Glu Tyr Glu Leu Glu Lys Asn His Val Glu Leu Arg Glu
351 225          230          235          240
354 Met Val Glu Glu Gly Tyr Asp Leu Leu Gly Thr Leu Asn Trp Thr Asp
355          245          250          255
358 His Leu Pro Trp Leu Ser Glu Phe Asp Pro Gln Arg Leu Arg Ser Arg
359          260          265          270
362 Cys Ser Thr Leu Val Pro Lys Val Asn Arg Phe Val Ser Arg Ile Ile
363          275          280          285
366 Ser Glu His Arg Asn Gln Thr Gly Asp Leu Pro Arg Asp Phe Val Asp
367          290          295          300
370 Val Leu Leu Ser Leu His Gly Ser Asp Lys Leu Ser Asp Pro Asp Ile
371 305          310          315          320
374 Ile Ala Val Leu Trp Glu Met Ile Phe Arg Gly Thr Asp Thr Val Ala
375          325          330          335
378 Val Leu Ile Glu Trp Ile Leu Ala Arg Met Val Leu His Pro Asp Met
379          340          345          350
382 Gln Ser Thr Val Gln Asn Glu Leu Asp Gln Val Val Gly Lys Ser Arg
383          355          360          365
386 Ala Leu Asp Glu Ser Asp Leu Ala Ser Leu Pro Tyr Leu Thr Ala Val
387          370          375          380
390 Val Lys Glu Val Leu Arg Leu His Pro Pro Gly Pro Leu Leu Ser Trp
391 385          390          395          400
394 Ala Arg Leu Ala Ile Thr Asp Thr Ile Val Asp Gly Arg Leu Val Pro
395          405          410          415
398 Ala Gly Thr Thr Ala Met Val Asn Met Trp Ala Val Ser His Asp Pro
399          420          425          430
402 His Val Trp Val Asp Pro Leu Glu Phe Lys Pro Glu Arg Phe Val Ala
403          435          440          445
406 Lys Glu Gly Glu Val Glu Phe Ser Val Leu Gly Ser Asp Leu Arg Leu
407          450          455          460
410 Ala Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Lys Asn Leu Gly
411 465          470          475          480
414 Phe Thr Thr Val Met Phe Trp Thr Ala Met Met Leu His Glu Phe Glu
415          485          490          495
418 Trp Gly Pro Ser Asp Gly Asn Gly Val Asp Leu Ser Glu Lys Leu Arg
419          500          505          510
422 Leu Ser Cys Glu Met Ala Asn Pro Leu Pro Ala Lys Leu Arg Arg Arg
423          515          520          525
426 Arg Ser
427          530
430 <210> SEQ ID NO: 4
432 <211> LENGTH: 15
434 <212> TYPE: DNA
436 <213> ORGANISM: artificial sequence

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VERIFICATION SUMMARY

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L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date